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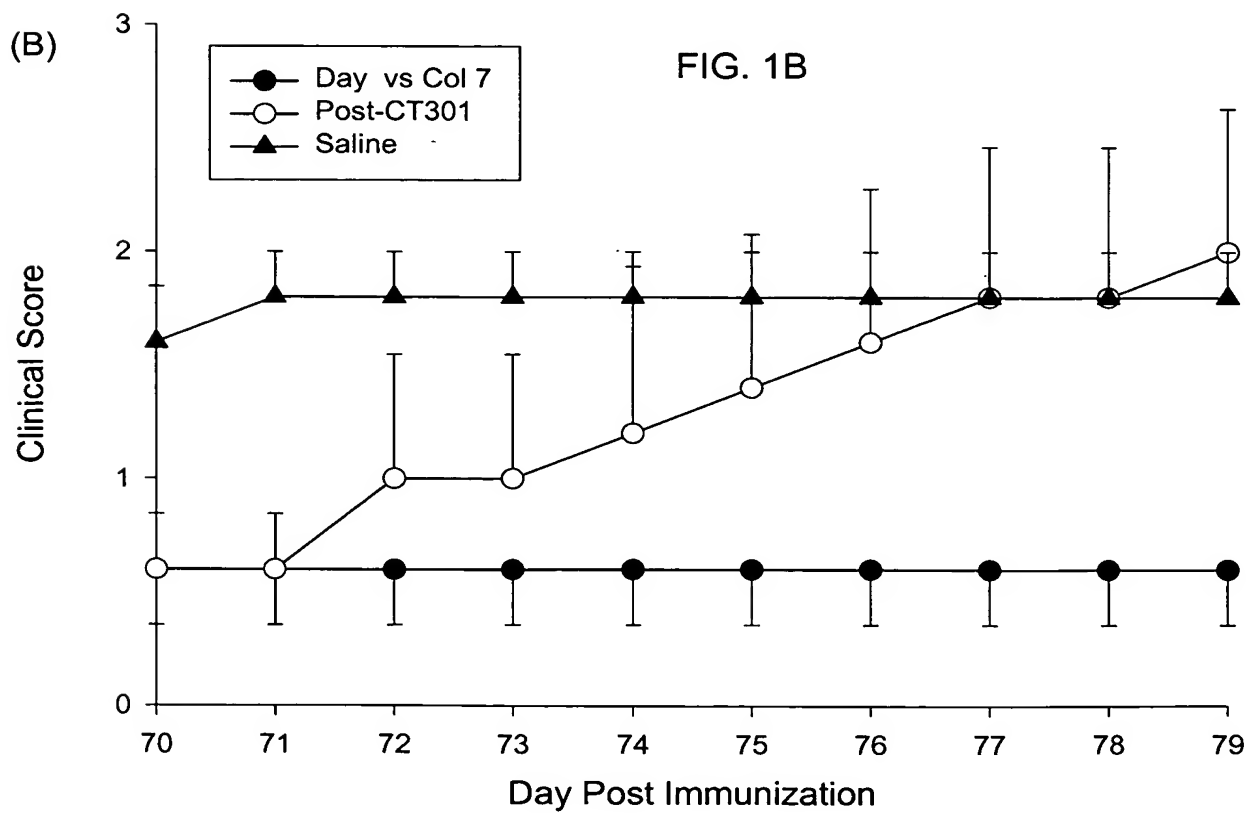
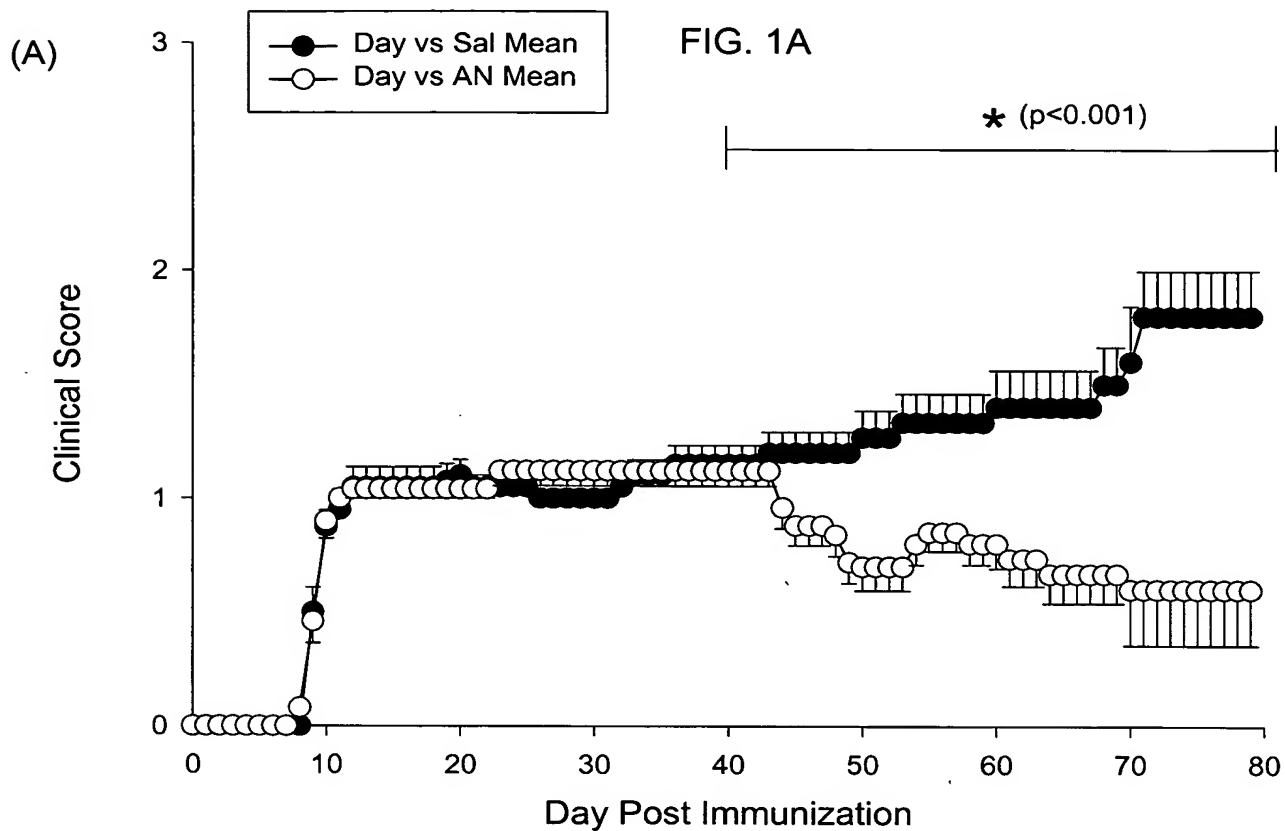




FIG. 2A

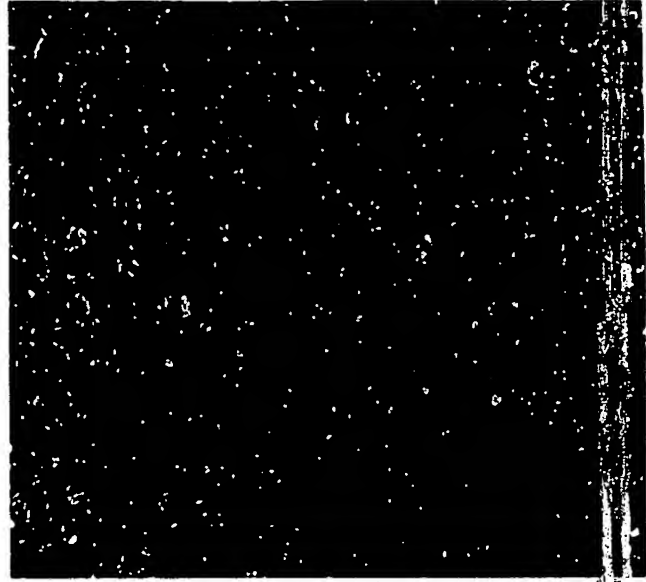


FIG. 2B



FIG. 2C

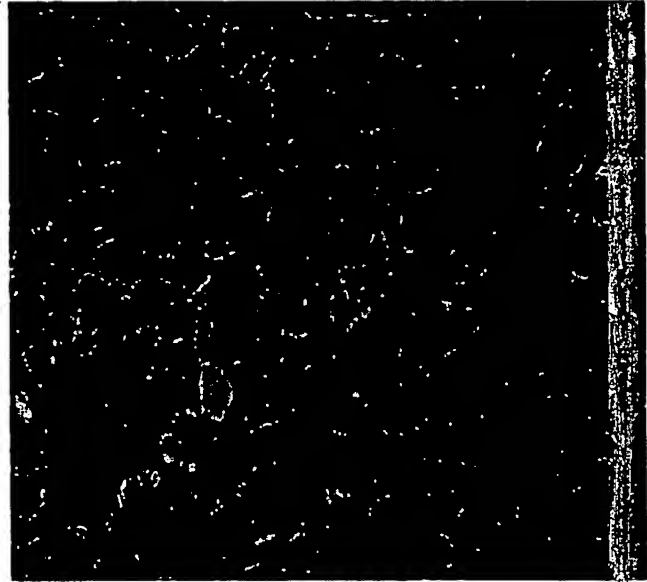


FIG. 2D



FIG. 2E

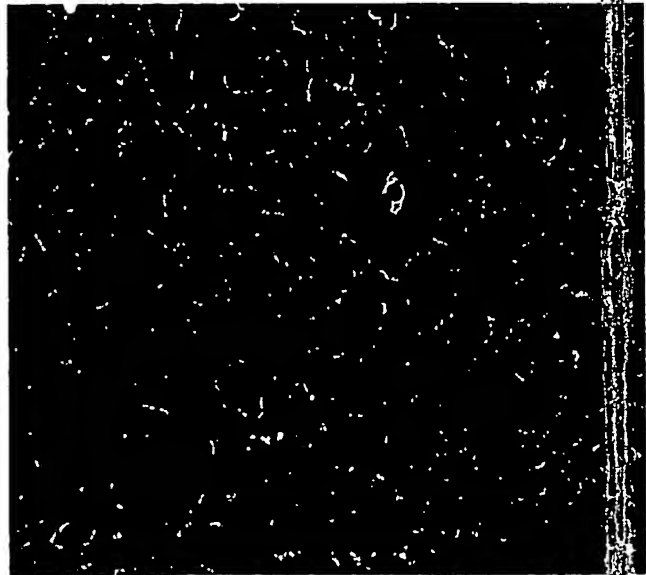


FIG. 2F



FIG. 2G

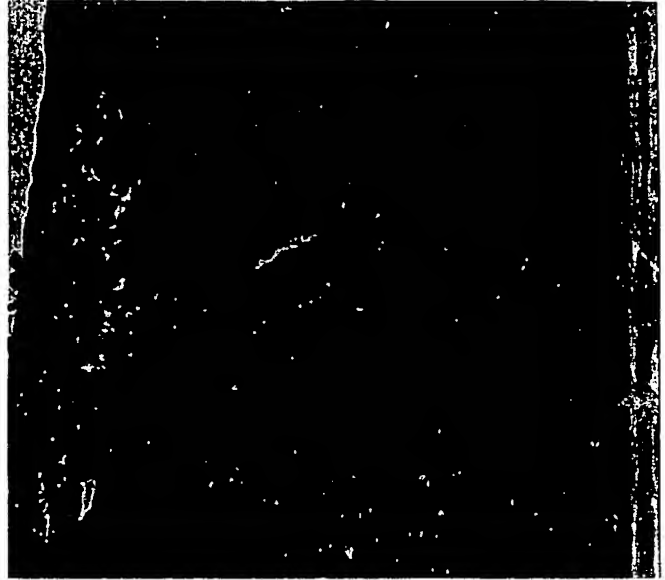


FIG. 2H

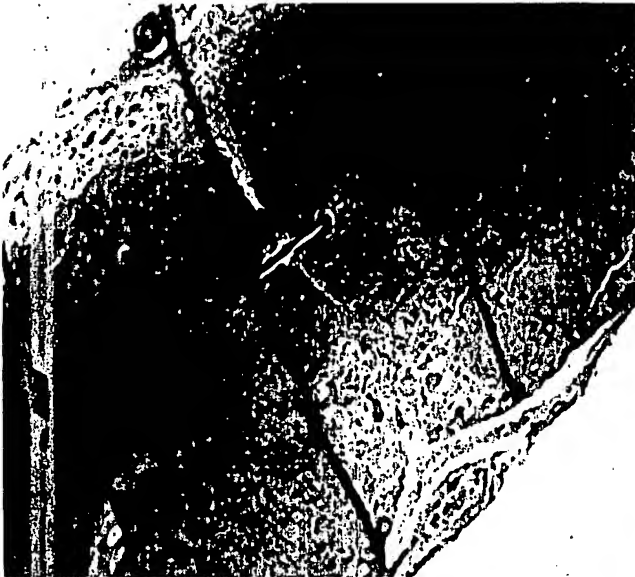


FIG. 2I



FIG. 2J

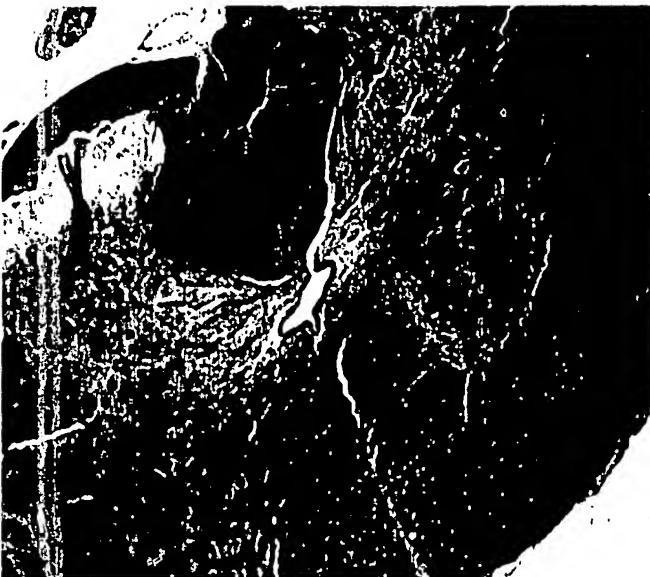
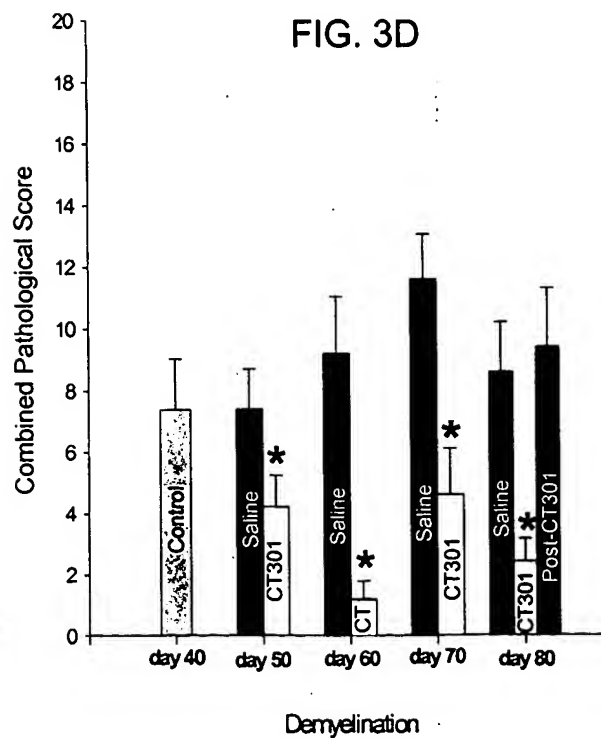
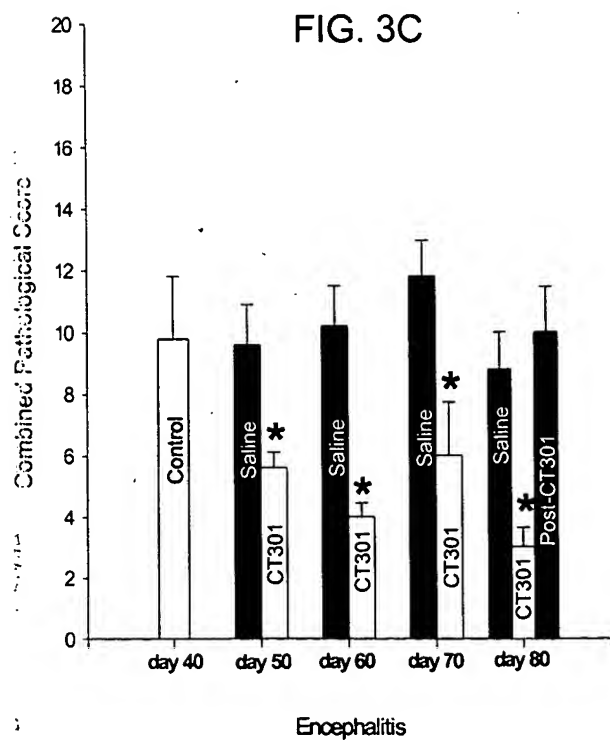
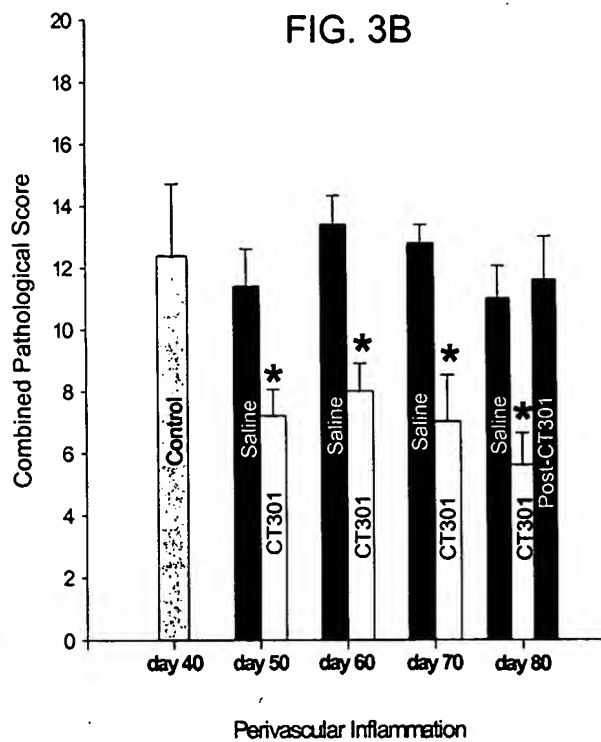
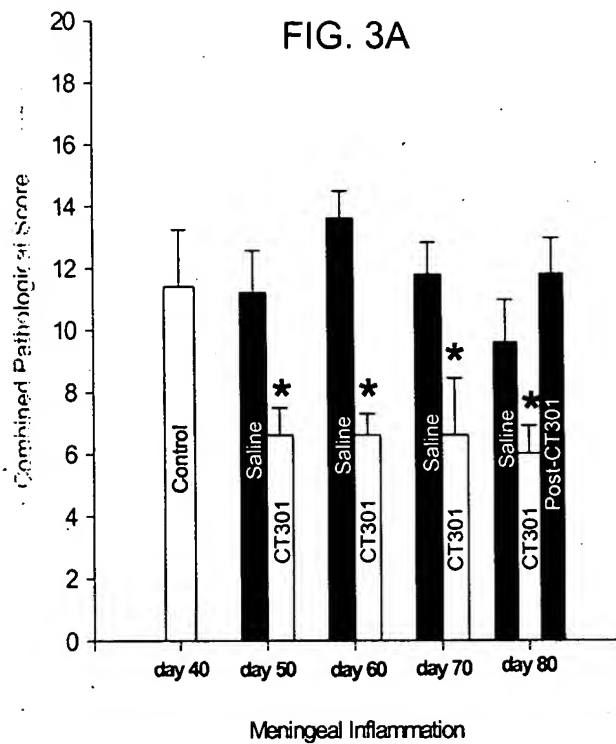


FIG. 2K



FIG. 2L



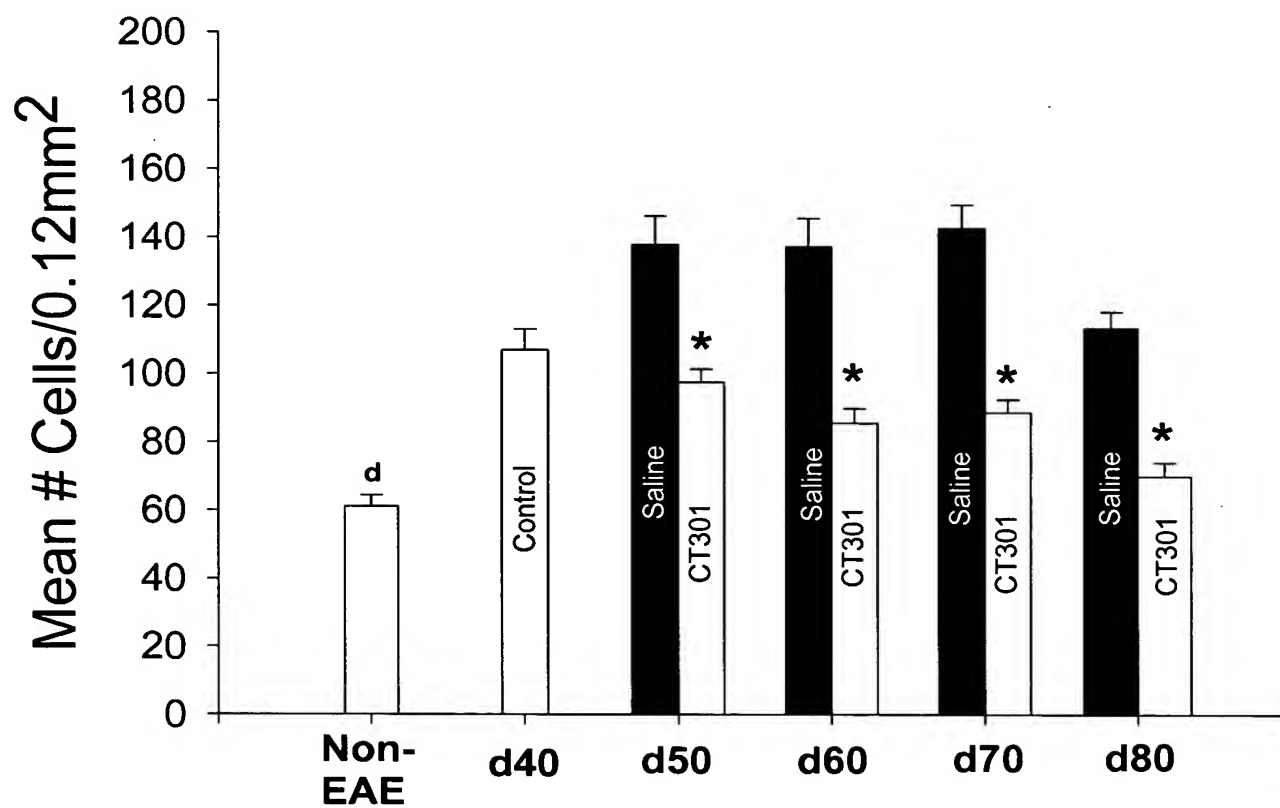
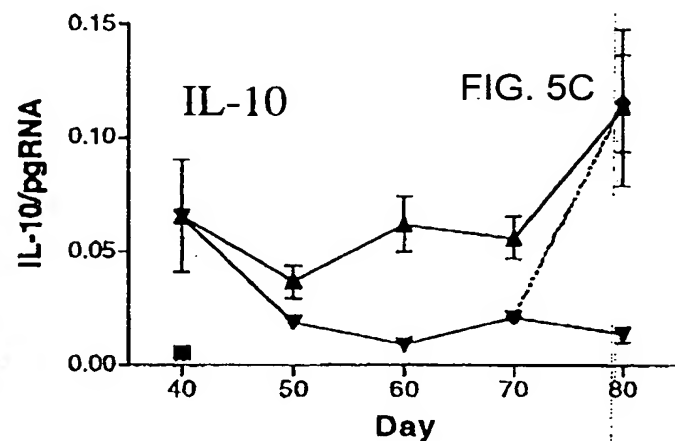
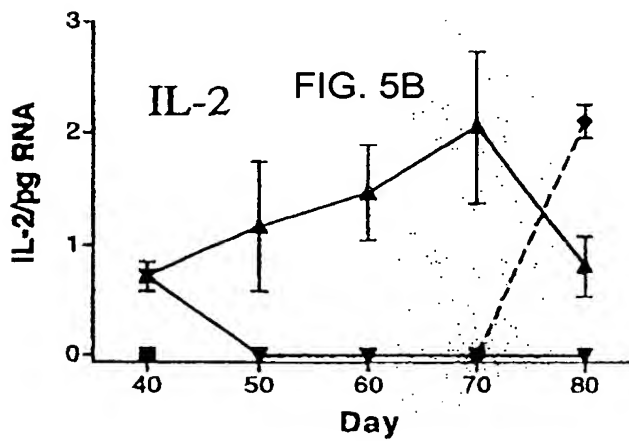
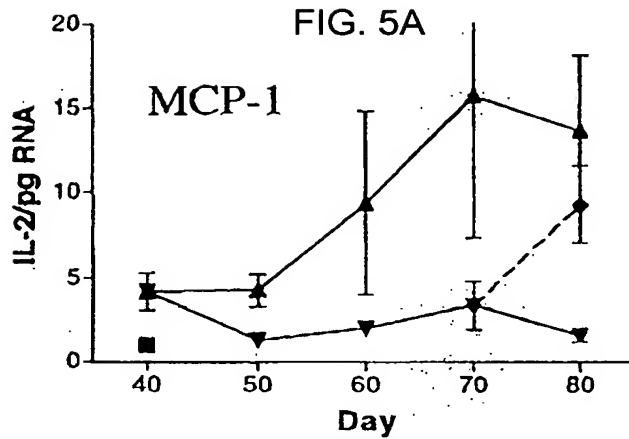
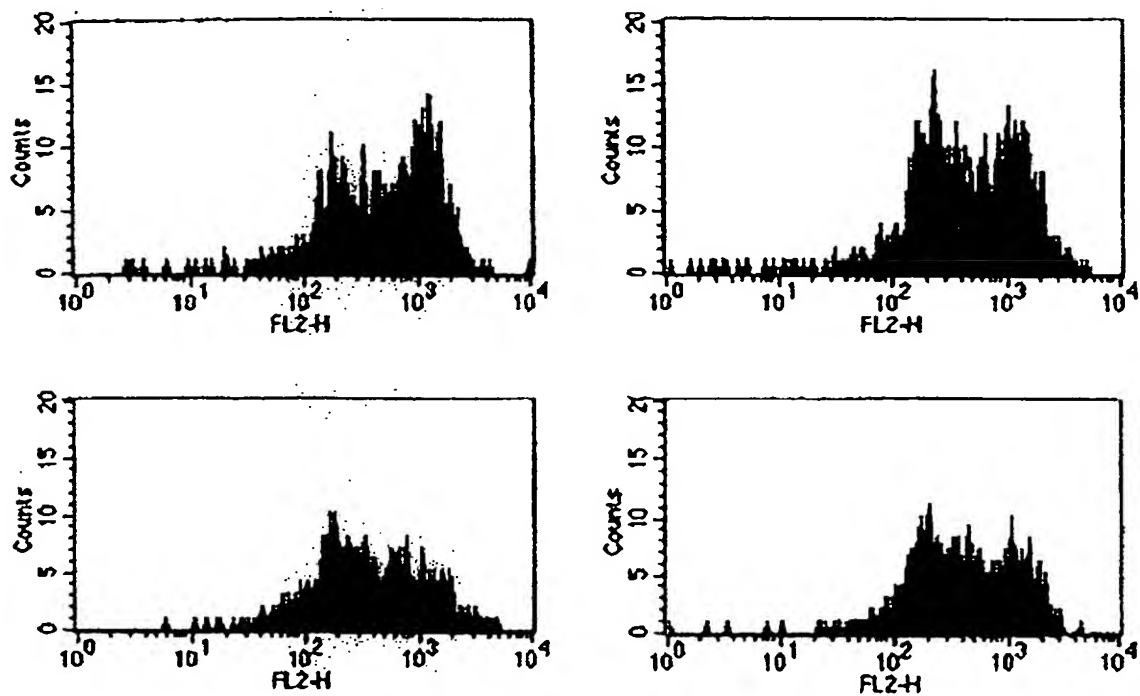


FIG. 4



CT301



Saline

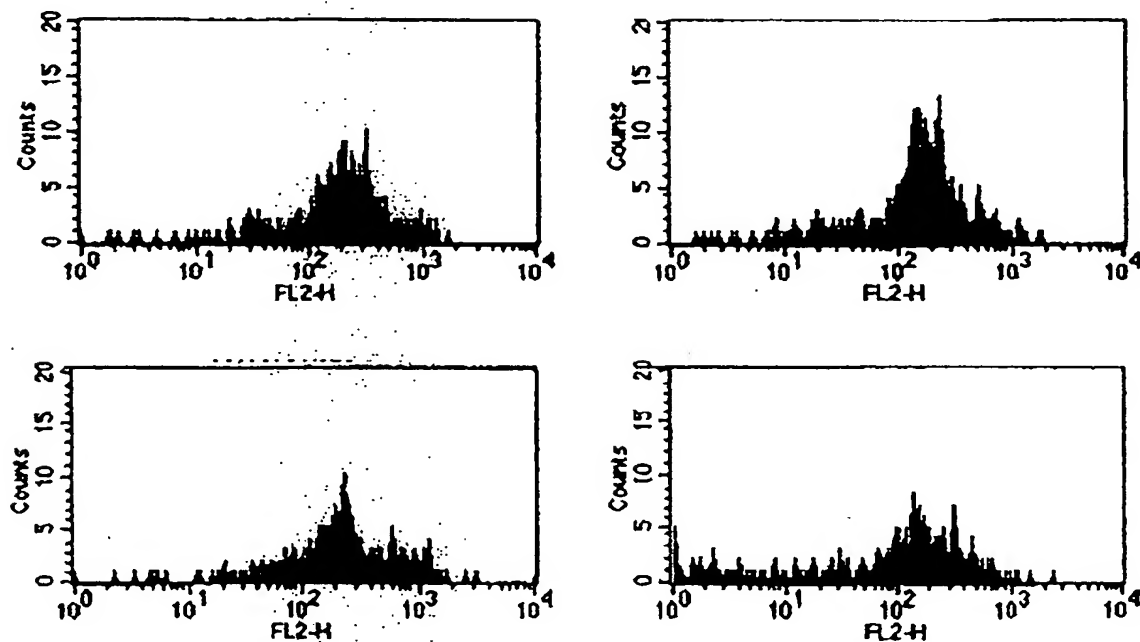


FIG. 6

Percentage $\alpha 4$ Integrin-High Blood Lymphocytes

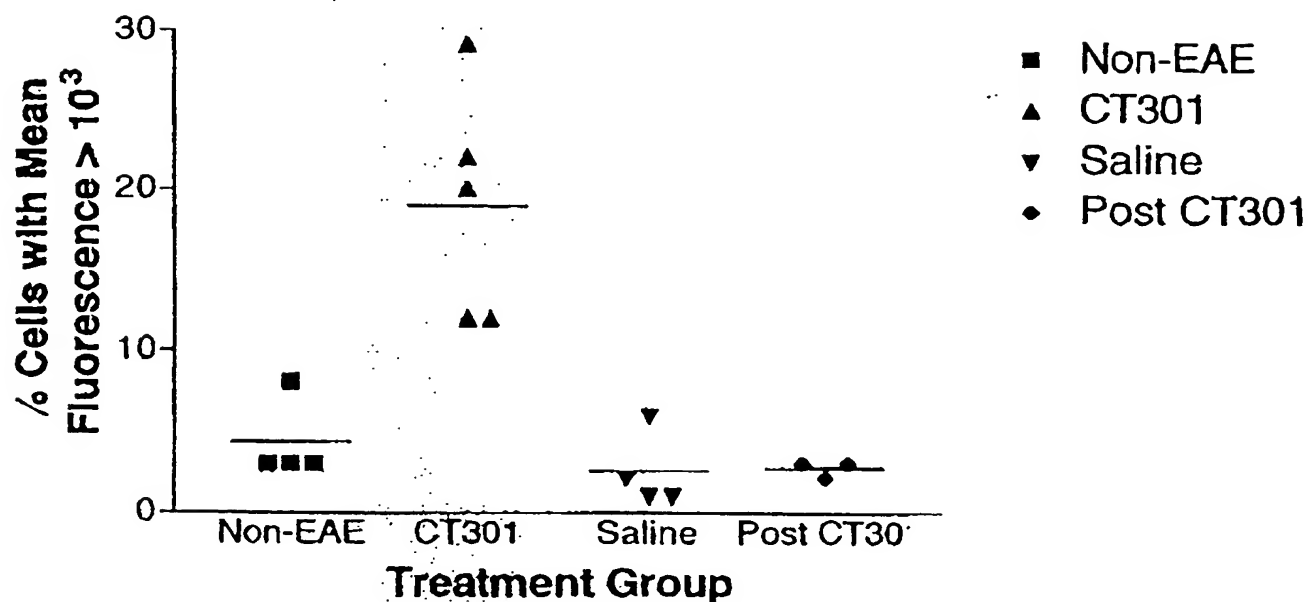


FIG. 7A

Expression of $\alpha 4$ Integrin on Blood Monocytes

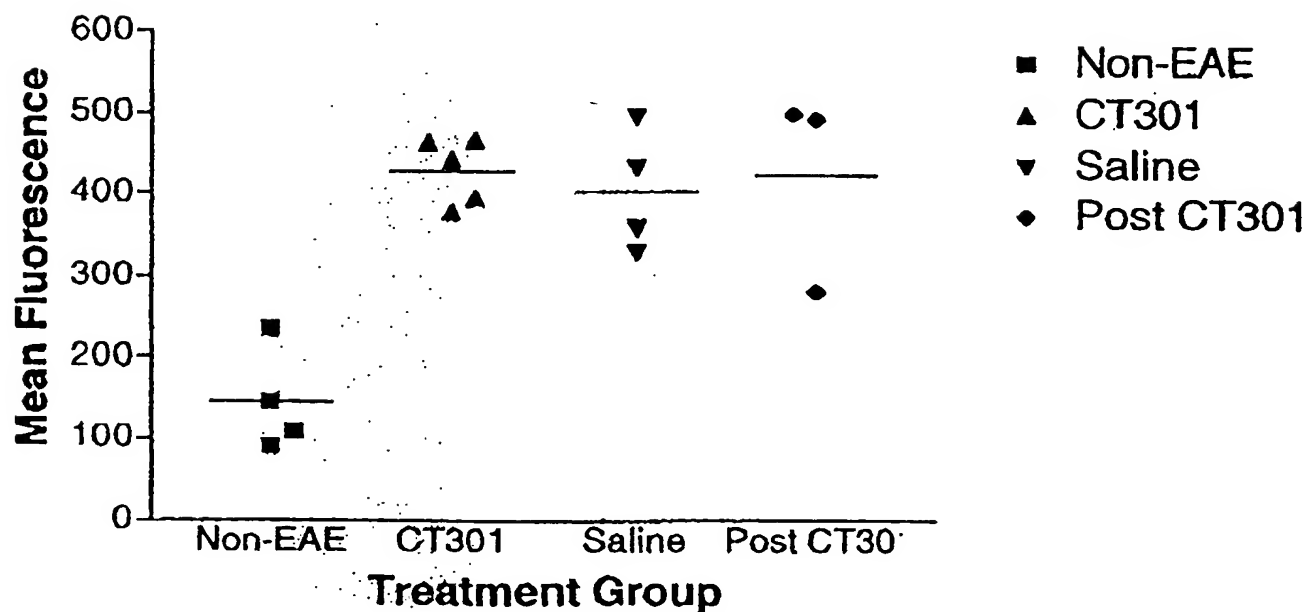


FIG. 7B

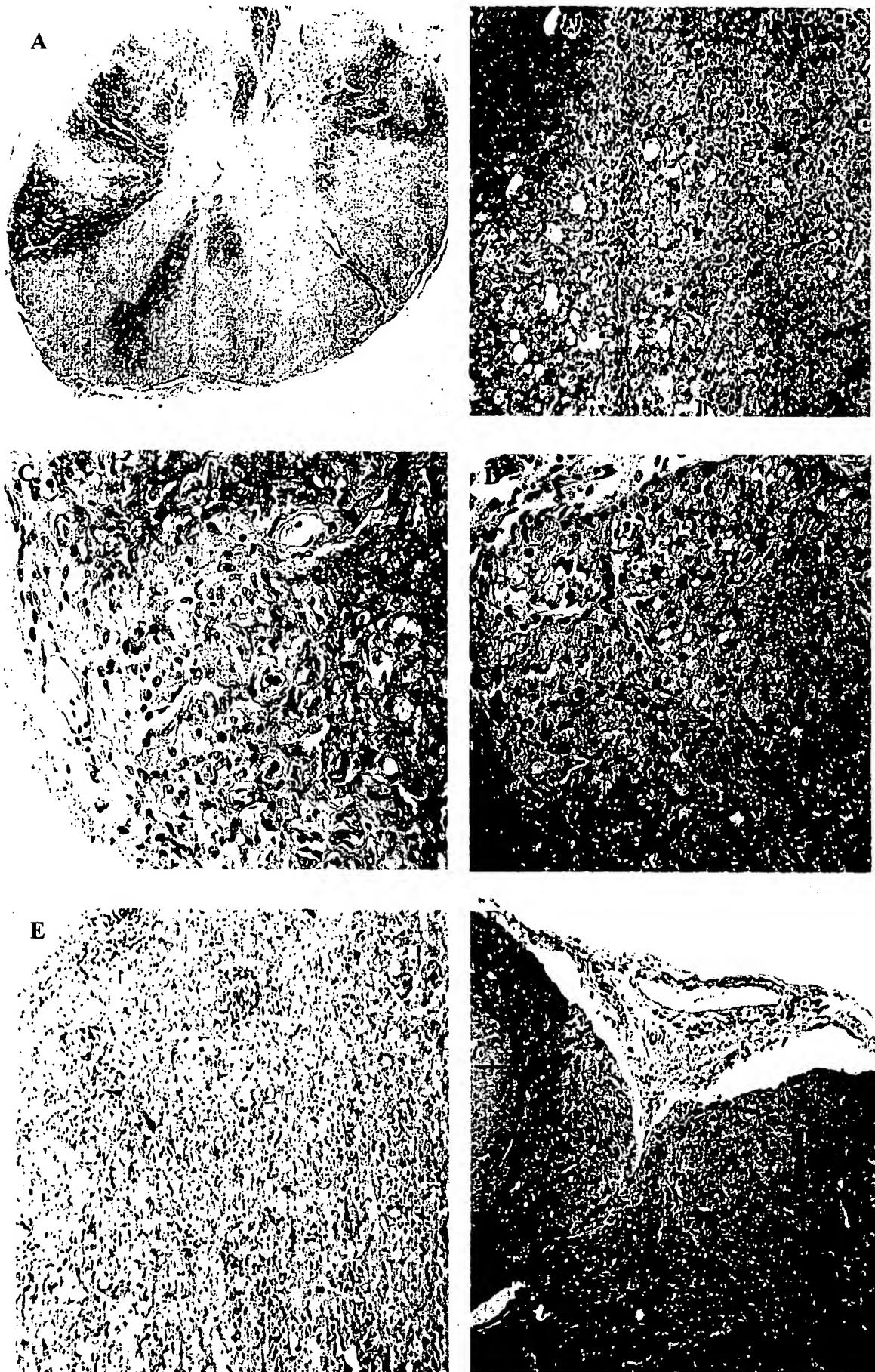


FIG. 8

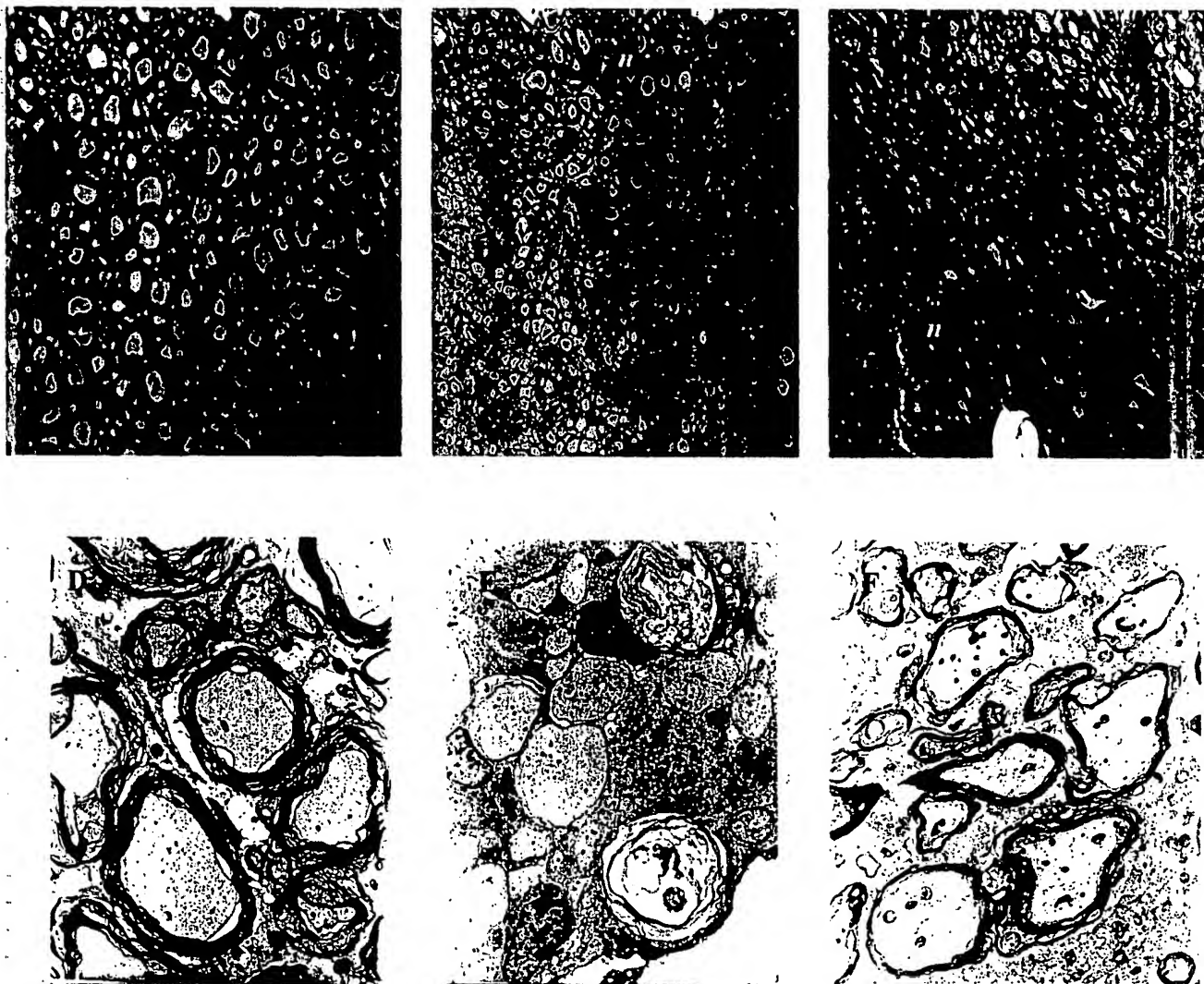


FIG. 9

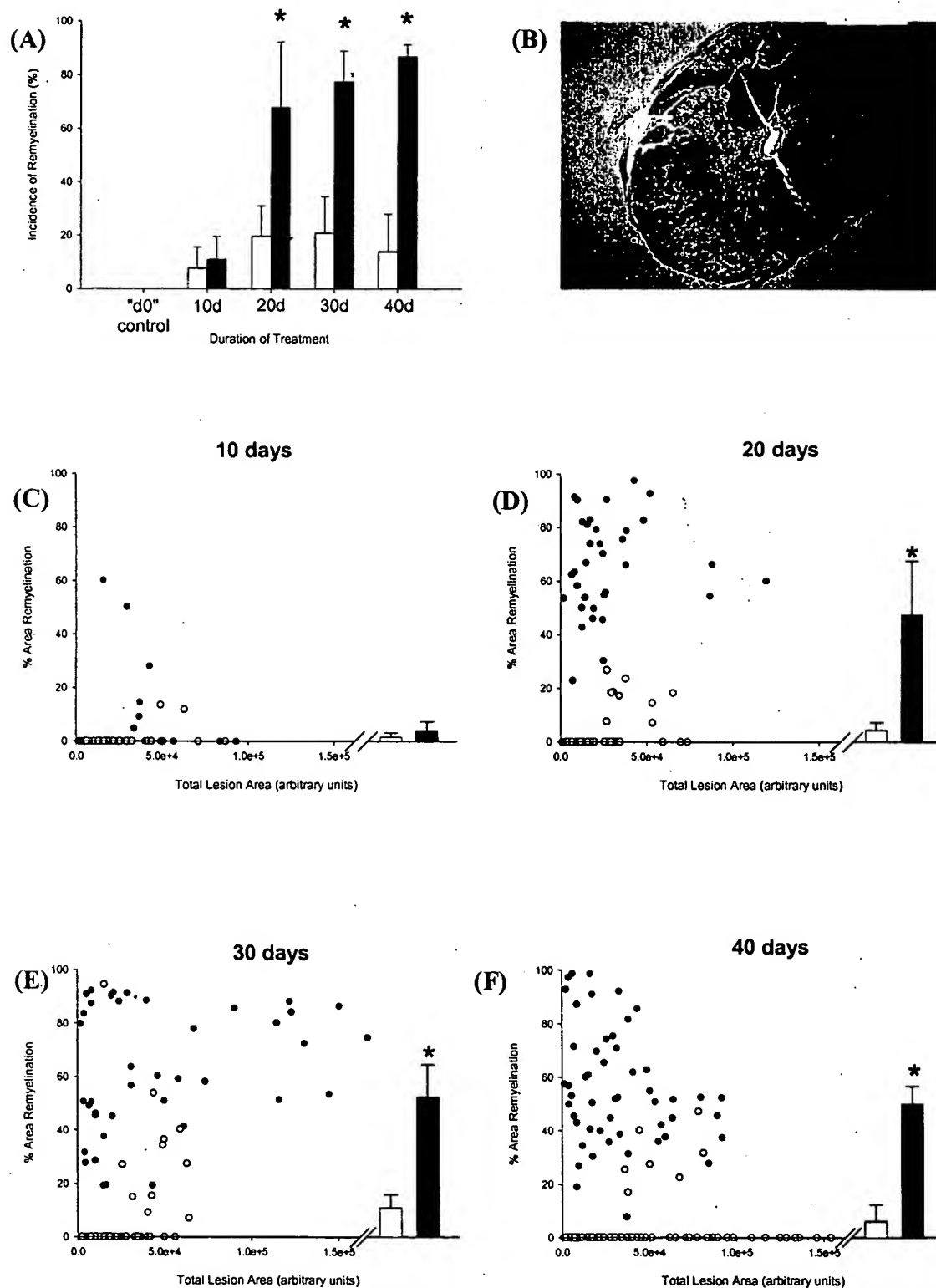


FIG. 10

1 atgagggccctgctcagatcttttggattcttggtcaggagacgttgt

tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca

49 agaaatgagaccgtctattcagttcctggggctcttgttgttctggcttcattg

tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

(M R P S I Q F L G L L L F W L H G
LEADER

103 tgctcagtgtagacatccagatgacacagttctccatcctcactgtctgcattctt

accagtcacactgtagggtctactgtgtcagaggtaggagtgacagacgtagaga

A Q C)[D I Q M T Q S P S S L S A S L
FR1

157 gggaggcaaagtccaccatcacttgcaagacaagccaagacattaacaagtatat

ccctccgtttcagtggttagtgaacgttctgttcggttctgtaattgttcataata

G G K V T I T C)[K T S Q D I N K Y M
CDR1

211 ggcttggtaccaacacaagcctggaaaacgtcctagggtgctcatacattacac

ccgaaccatggttgtgttcggaccttttgcaggatccgacgagtatgtaattgtg

A)[W Y Q H K P G K R P R L L I H)[Y T
FR2

265 atctgcattacagccaggcatcccatcaagggttcagtggaagtgggtctgggag

tagacgtaattgtcgggtccgtagggttagttccaagtcaccttcacccagaccctc

S A L Q P)[G I P S R F S G S G S G R
CDR2

FIG. 11 A

319 agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta

tctaataaggaagttgtagtcggtggacctcggacttctataaacggtgaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

373 ttgtctacagtatgataatctgtggacggttcggtggaggcaccaagctggaaat

aacagatgtcatactattagacacctgcaagccacctccgtgggttcgaccttta

C)[L Q Y D N L W T][F G G G T K L E I
CDR3 FR4

427 caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga

gtttgcccgactacgacgtgggtgacataggtagaagggtaggtgggcctt

K]

AGG-5'
tcc
481 ---
agg

FIG. 11B

1 atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg

tactttacgtcgacccagtcacaagaaggactaccgtcaccaatgtccc

[M K C S W V M F F L M A V V T G
LEADER

49 gtcaattcagaggttcagctgcagcagtcctggggcagagcttgtgaagccaggg

cagttaagtctccaagtcgacgtcgtcagaccccgctcgaacacttcgggtccc
V N S)[E V Q L Q Q S G A E L V K P G
FR1

103 gcctcagtcgaagttgtcctgcacagcttctggcttcaacattaaagacacctat

cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata
A S V K L S C T A S G F N I K)[D T Y
CDR1

157 atacactgtgtgaagcagaggcctgaacagggcctggagtggttggaaggatt

tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa
I H)[C V K Q R P E Q G L E W I G)(R, I
FR2

211 gatcctgcgaatggttataactaaatatgacccgaagttccagggaaggccact

ctaggacgcttaccaatatgatttatactgggcttcaagggtcccgttccgggtga
D P A N G Y T K Y D P K F Q G)(K A T
CDR2

265 ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca

tattgtcgactgtgtaggaggttgtgtcggtatggacgtcgagtcgtcggactgt
I T A D T S S N T A Y L Q L S S L T
FR3

FIG. 12A

319 tctgaggacactgccgtctatttctgtgctagagaggatattatggtaactac

agactcctgtgacggcagataaagacacgatctctccctataataaccattgatg
S E D T A V Y F C A R][E G Y Y G N Y
CDR3.

373 ggggtctatgctatggactactgggggtcaaggaacctcagtcaccgtctcctca

ccccagatacagataacctgatgaccccagttccttggagtcagtggcagaggagt
G V Y A M D Y][W G Q C T S V T V S S]

427 gccaaaacgacacccccatctgtctatccactggcccgggatcc

cggtttttgctgtgggggtagacagataggtgaccgggcctagg
S S]

FIG. 12B

	FR1		CDR1		FR2		CDR2
	1	2	3		4		5
	12345678901234567890123	45678901234	5678901234		567890123456789		0123456
	*		*****		*		***
21.6	DIQMTQSPSSLSASLGGKVTITC	KTSQDINKYMA	WYQHKPGKRPRLLIH		YTSALQP		
REI	DIQMTQSPSSLSASVGDRVITC	QASQDIKYLN	WYQQTGKAPKLLIY		EASNLQA		
La	DIQMTQSPSSLSASVGDRVITC	KTSQDINKYMA	WYQQTGKAPRLLIH		YTSALQP		
Lb	-----R-----						

	FR3		CDR3		FR4
	6	7	8	9	10
	78901234567890123456789012345678	901234567	8901234567		
	*	*	*****		
21.6	GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC	LQYDNL-WT	FGGGTKLEIK		
REI	GVPSRFSGSGSGTDYFTISSLQPEDATYYC	QQYQSLPYT	FGQGTLQIT		
La	GIPSRFSGSGSGRDYFTISSLQPEDATYYC	LQYDNL-WT	FGQGTKVEIK		
Lb	-I-----R-----VE-K				

FIG. 13

	FR1									CDR1					FR2					CDR2				
	1			2			3			4			5			6								
	123456789012345678901234567890	12345	67890123456789012345	67890123456789	012A3456789012345																			
	*****									***					****									
21.6	EVQLQQSGAELVKPGASVKLSCTASGFNIK DTYIH CVKQRPEQGLEWIG RIDPANGYTKYDPKFQG																							
2*CL	QVQLVQSGAEVKKPGASVKVSCKASGYTFT SYAMH WVRQAPGQRLEWMB WINAGNGNTKYSQKFQG																							
Ha	QVQLVQSGAEVKKPGASVKVSCKASGFNIK DTYIH WVRQAPGQRLEWMB RIDPANGYTKYDPKFQG																							
Hb	-----FNIK -----G-----																							
Hc	-----FNIK -----																							

	FR3												CDR3				FR4			
	7			8			9			10			11							
	67890123456789012ABC345678901234	567890ABCDEF12	34567890123																	
	*												*							
21.6	KATITADTSSNTAYLQLSSLTSED TAVYFCAR EGYYGNYGVYAMDY WGQGTSVTVSS																			
2*CL	RVTITRDTSASTAYMELSSLRSED TAVYYCAR GGYGSGS----NY WGQGLTVTVSS																			
Ha	RVTITADTSASTAYMELSSLRSED TAVYYCAR EGYYGNYGVYAMDY WGQGLTVTVSS																			
Hb	-----A-----																			
Hc	-----A-----F-----																			

FIG. 14

HindIII KOZAK SEQUENCE
aagccttgcgccaccargagaccgtctattcagttcctggggctcttggtgttc
1 -----
ttcgaacggcggtggtactctggcagataagtcaaggaccccgagaacaacaag
[M R P S I Q F L G L L L F
LEADER
tggcttcattggtgctcagtggtgacatccagatgacacagttctccatcctcactg
55 -----
accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgc
W L H G A Q C][D I Q M T Q S P S S L
FR1
tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt
109 -----
agacgtagaCATcctCTATCTcagtggtagtgaacggttctgttcggttctgtaa
S A S V G D R V T I T C][K T S Q D I
CDR1
aacaagtatatggccttggtaccaaCAGACAcctggaaaaGCTcctagggtgctc
163 -----
ttgttcataataccgaaccatgggtGTCTGTggaccttttCGAggatccgacgag
N K Y M A)[W Y Q Q T P G K A P R L L
FR2
atacattacacatctgcattacagccaggcatcccatcaagggttcagtggaagt
217 -----
tatgtaatgtgtagacgtaatgtcggtccgtagggtagttccaagtcaccttca
I H)[Y T S A L Q P][G I P S R F S G S
CDR2
gggtctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt
271 -----
cccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa
G S F R D Y T F T I S S L Q P E D I
FR3

FIG. 15A

325 gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc

cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg
A T Y Y C)[L Q Y D N L W T][F G Q G T
CDR3 FR4

SPLICE DONOR SITE BamHI
aagGTGgaaatcaaacgtgagtgatcc
379 -----
ttcCACctttagtttgcactcacctagg
K V E I K]

FIG. 15B

HindIII KOZAK SEQUENCE

1 AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG

TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAACGGACGAGCGGCAC
[M D W T W R V F C L L A V
LEADER
55 GCTCCTGGGGCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG

CGAGGACCCCGGGTGTCTGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC
A P G A H S][Q V Q L V Q S G A E V K
109 AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa

TTTGGGCCACGAAGGCACTTTTCAGTCGACATTTTCGATCGCCAaagttgtaattt
K P G A S V K V S C K A S G F N I K][
FR1
163 gacacctatatacactGGGTTAGACAGGCCCCctGGCCAAaGGCTgGAGTGGATg

ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAC
D T Y I H][W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 16A

217 GGaaggattgatcctgcgaatggttataactaaatatgacccgaagttccagggc

CCTtcctaactaggacgcttaccaatatgattttatactgggcttcaaggtcccg
G)[R I D P A N G Y T K Y D P K F Q G)]
CDR2

271 cgggtcACcAtcACCgcaGACACCTCTgccagcACCGCCTACATGGAAGTGTCC

gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG
R V T I T A D T S A S T A Y M E L S
FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat

TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata
S L R S E D T A V Y Y C A R)](E G Y Y
ggtaactacggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTcACC
379 -----
ccattgatgccccagatacagatacCTGATgACCCCaGTtCCtTGGGAACAGTGG
G N Y G V Y A M D Y)](W G Q G T L V T
CDR3 FR4

SPLICE DONOR SITE BamHI
433 GTcTcctCAGGTGAGTGGATCC

CAGaggAGTCCACTCACCTAGG
V S S]

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B